IN THE SPECIFICATION:

Please replace the paragraph beginning at page 4, line 25, with the following rewritten paragraph:

a1

– Figures 1A-1C (SEQ ID NO:1) show an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BFA4. The start and stop codons are shaded, designating an open reading frame. The underlined sequence corresponds to that of accession no. AA428090. –

Please replace the paragraph beginning at page 5, line 1, with the following rewritten paragraph:

a2

– Figure 2 (SEQ ID NO:2) shows an embodiment of an amino acid sequence of BFA4. –

Please replace the paragraph beginning at page 6, line 12, with the following rewritten paragraph:

a3

– In a preferred embodiment, the breast cancer sequences are those of nucleic acids encoding BFA4 or fragments thereof. Preferably, the breast cancer sequence is that depicted in figures 1A-1C (SEQ ID NO:1), or a fragment thereof. Preferably, the breast cancer sequences encode a protein having the amino acid sequence depicted in figure 2 (SEQ ID NO:2), or a fragment thereof. In a preferred embodiment, the breast cancer sequences encode human zinc finger transcription factor TRPS1.–

Please replace the paragraph beginning at page 11, line 24, with the following rewritten paragraph:

a4

– The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. For example, cytokine receptors are characterized by a cluster of cysteines and a WSXWS (W= tryptophan, S= serine, X=any amino acid) motif (SEQ ID NO:3). Immunoglobulin-like domains are highly conserved. Mucin-like domains may be involved in cell adhesion and leucine-rich repeats participate in protein-protein interactions. –

Please replace the paragraph beginning at page 13, line 12, with the following rewritten paragraph:

a5

– In a preferred embodiment, the sequences which are used to determine sequence identity or similarity are selected from the sequences set forth in the figures, preferably that shown in Figures 1A-1C (SEQ ID NO:1) and fragments thereof. In one embodiment the sequences utilized herein are those set forth in the figures. In another embodiment, the sequences are naturally occurring allelic variants of the sequences set forth in the figures. In another embodiment, the sequences are sequence variants as further described herein. –

Please replace the paragraph beginning at page 14, line 4, with the following rewritten paragraph:

a6

– Thus, "percent (%) nucleic acid sequence identity" is defined as the percentage of nucleotide residues in a candidate sequence that are identical with the nucleotide residues of figures 1A-1C (SEQ ID NO:1). A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively. –

Please replace the paragraph beginning at page 42, line 10, with the following rewritten paragraph:

a7

– In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular breast cancer gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of breast cancer genes are sometimes referred to herein as "breast cancer proteins" or "breast cancer modulating proteins" or "BCMP". Additionally, "modulator" and "modulating" proteins are sometimes used interchangeably herein. In one embodiment, the breast cancer protein is termed BFA4. BFA4 sequences can be identified as described herein for breast cancer sequences. In one embodiment, a BFA4 protein sequence is as depicted in Figure 2 (SEQ ID NO:2). The breast cancer protein may be a fragment, or alternatively, be the full length protein to the fragment shown herein. Preferably, the breast cancer protein is a fragment. In a preferred embodiment, the amino acid sequence which is used to determine sequence identity or similarity is that depicted in figure 2. In another embodiment, the sequences are naturally occurring allelic variants of a protein having the sequence depicted in figure 2. In another embodiment, the sequences are sequence variants as further described herein. –

inserted as a8

On page 61, immediately preceding the claims, please insert the enclosed text entitled "SEQUENCE LISTING".